ECORIA

24

39

54

GAATTCCGG TGC AGG ACG AAG CTG TTC TGG ATT TCT TAC AGT GAT GGG GAC CAG
Arg Thr Lys Leu Phe Trp 11e Ser Tyr Ser Asp Gly Asp Gln

69
TGT GCC TCA AGT CCA TGC CAG AAT GGG GGC TCC TGC AAG GAC CAG CTC CAG TCC
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser

114 129
TAT ATC TGC TTC TGC CTC CCT GCC TTC GAG GGC CGG AAC TGT GAG ACG CAC AAG TTY ITE Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys

PST IA

174

189

GAT GAC CAG CTG ATC TGT GTG AAC GAG AAC GGC GGC TGT GAG CAG TAC TGC AGT
ASP ASP GIn Leu lie Cys Val Asn Glu Asn Gly Gly Cys Gin Gin Tyr Cys Ser

279 294 309 324
GCA GAC GGG GTG TCC TGC ACA CCC ACA GTT GAA TAT CCA TGT GGA AAA ATA CCT
Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys lle Pro

Xba I 339
ATT CTA GAA AAA AGA AAT GCC AGC AAA CCC CAA GGC CGA ATT GTG GGG GGC AAG
ILE LEU GTU Lys Arg Asn Ala Ser Lys Pro Gin Gly Arg Ile Val Gly Gly Lys

384
399
GTG TGC CCC AAA GGG GAG TGT CCA TGG CAG GTC CTG TTG TTG GTG AAT GGA GCT
Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala

444 459
CAG TTG TGT GGG GGG ACC CTG ATC AAC ACC ATC TGG GTG GTC TCC GCG GCC CAC
Gln Leu Cys Gly Gly Thr Leu lle Asn Thr lle Trp Val Val Ser Ala Ala His

489 504 504
TGT TTC GAC AAA ATC AAG AAC TGG AGG AAC CTG ATC GCG GTG CTG GGC GAC CAC
Cys Phe Asp Lys lie Lys Asn Trp Arg Asn Leu lie Ala Val Leu Gly Glu His

549

GAC CTC AGC GAG CAC GAC GGG GAT GAG CAG AGC CGG CGG GTG GCG CAG GTC ATC
ASP Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val lle

639

ATC CCC AGC AGG TAC GT<u>C CCG GG</u>C ACC ACC AAC CAC GAC ATC GCG CTG CTC CGC lle Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg

654
669
669
654
CTG CAC CAG CCC GTG GTC CTC ACT GAC CAT GTG GTG CCC CTC TGC CTG CCC GAA
Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu

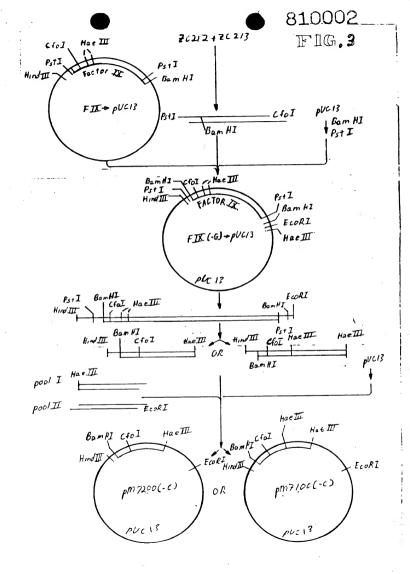
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			-60 	1 = 8 1 = 1 = mikr			IvLouG1 nG		41-61-61-61	olaleLyeal	eSer61y
AACAGGCAGGGGC	ACCACTGCAG	AGATTTCATC	TESTCTOOC	AGGCCCTCAG	COTOCTCTGO	тспьстть	CCCTTCAGG	CTGGCTGGCT	CONCECCE	TOGCTANGGO	CTCACCA
10	20	30	€0	, 5 0	-	70 ·10	80		100 •1	110	120
-20 61yG1uThrArgA			-20				a I I aw Wil a A		41-441-4	PhoLouG1uG1	uLouire
61yG1uThrArgA 66AGAAACACGGG	apHetProTr	pLyaProG19	Profitences Profitences	TCTTCTTAC	CAGGAGGAAG	CCCACCCC	TOCTGCACO		COCTROPOCO.	TTOCTGGAGGA	ECTEGE
130	140	150	160	170	100	190	200			230	240
•10		+20			•30		1-61-47	+40 hri val auPha	2T1-4	TvrSerAssG	vAepGlo
+10 ProGlySerLeuG COGGGCTCCCTGG	luArgGluCy	elysGluGlu	61nCyeSeri	PheGluGluAl	AUCCCOCOCOLOGICAL COLO	TTCAAGGAC	CEGAGAGGA	CGAAGCTGTTC	TEGATTTET	TACACTGATG	CCACCAC
250	260	270	280	290			320			250	360
•90		+60)		+70			• 8 0		Htal valent	anG1 al.es
+50 CynAleSerSer! TGTGCTCAAGTC	ProCyeG1nA	anG1yG1ySet	CycLychop	GlnLeuGlnSe	or Tyr IleCyal	PhoCysleui Traccation	770818F786	ACCCCCCCCCAAC	TETEAGAGE	CACAAGGATG	ACCAGCTE
TGTGCCTCAAGTC	DCATGCCAGA: 280	890	400	410	420	430	440	450	460	470	480
					+110			+120			
+90 IleCysVelAsm ATCTGTGTGAAC	GlukanGlyG	1yCyaG1aG1	TyrCyaSer	AspHieThrG	lyThrLyeArg	SerCyeAry TOTAL	rcocentraci	COTACTCTCT	CTGGCAGAC	EGGTGTOCT	SCACACOC
ATCTGTGTGANO	GAGAACCGCG	OC 10 I MINOR	STACTSCAGT	GACCACACGG S30	540	550	360	570	560	590	600
490 +130		510 +14						+164	0		
	ProCyaG1yL			ArgionAleS	erLysProGla	GlyArgI10	Ve1G1yG1yl	ysVelCysPT	oLy 8 617611	SCYBPECTEPS CTCTCCATGGC	ACCTOCTO
Thr VelGluTyr	CCATCTCCAA	MAATACCIAI	ICI NORMAN		GCAAACCCCAA 660	670	680	690	700	710	720
610	620	630	640	630			•••	420	^		
+170 LeuLeuVelAsn	~1~41~61ml			AanThrileT	rpVelVelSer	-AleAleHis	CyaPheAspi	LyallaLyaAs	n T rpårgås	nLouIleAla\	elleu619
TTGTTGCTGAAT	GENECTORE	1161616666					TETTTOGAC	B10	CTGGAGLAM 820	A30	840
730	760	750	760	770	/60			424	•		
+210 Sluits Aspley				ArevelAleG			TyrVelPro	GlyThrThrAs	nHieAspli	ek) ekoukou	rgloulie
GAGCAGGACCTC	AGOGAGCAC	ACCCCCATGA	CCAGAGOOG					EGCACCACCAA	OCACGACAT	OSOSCITICATOR	MACO TACON
850	860	870	880	-50				-20			
+250 GlnProVelVel		+26					41ePheVel	4 PA - BARI A	www.learci	yTrpG1yG1nl	outoute
GinProVelVel CAGCCCGTGGTC	LeuThraspi	CATCTCCTCC	CONTENED	COCCAACGG	COTTCTCTGA	CACCACCCTO				CTGGGGGCAG	CTECTEGA
970	980	990	1000	1010	1020	1000	1040	1050		1070	1000
+290		+30	00		+31	0			-Protenii	aThrG1uTvr	Hart Black
+290 ArgGlyAlaTh	rAleLeuGlu	LouisetVelle	euAssVelPr	cargiouliet'	ThrG1nAspCy ACCCAGGACTG	aLeuGl mG 11 CCTGCAGCAI	Ser Arglys STCACGG AAG	GTGGGAGACTC	COCAAATAT	CACGGAGTAC	ATGTTCTE
CETEGOGOCAC	GGCCCTGGAG	CTCATGGTGC	CARCE TOCO	oArgLeuNet' CCGGCTGATG 1130	1140	1150	Ser ArgLys STCACGGAAG 1160	1170	1180	CACGGAGTAC 1190	1200
1090 -230	1100	1110	1120 60	1130	1140	1150	1160	1170	1180 50	1190 	1200 G1=Cre41
1090 -230	1100	1110	1120 60	1130	1140	1150	1160	1170	1180 50	1190 	1200 G1=Cre41
1090 +330 AlaGiyTyr5a GOOGGTACTO	1100 rapglyser ggatggcagc	1110 +3- LyaAspSerC AAGGACTOCT	1120 60 yalyaGlyAa GCAAGGGGGA	1130	1140 +35 ProHisAleTh CCACATGCCAC 1260	1150 io irHieTyrAr ioCACTACCE 1270	1160	1170 +36 TyrLauThrG: TACCTGACGGG	1180 50 1y11eVe13e 5CATCGTCAG 1300	1190 erTrpG1yG1m ecTGGGGCCAG 1210	1200 G1YCYaA1 GGCTGCGC 1320
00166050CA0 1090 +330 AleG1yTyr3e 60056CTACTO 1210 +370	1100 rAspG1y3er GGATGGCAGC 1220	1110 +3- LyaAspSerC AAGGACTCCTI 1230 +3	1120 40 yalyaGlyAa GCAAGGGGGA 1240 80	1130 pSerGlyGly CAGTGGAGGO 1250	1140 +35 ProHisAleTh CCACATGCCAC 1260 +39	1150 orHieTyrar ocactacce 1270	1160 gGlyThrTrg GGGCACGTGG 1280	1170 +36 TyrLauThr61 TACCTGACGG 1290 +46	1180 50 LylleVelSe 5CATCGTCAC 1300 00	1190 orTrpG1yG1n ocTGGGGCCAG 1310 +406	1200 GlyCyall GGCTGCGC 1320
00166050CA0 1090 +330 AleG1yTyr3e 60056CTACTO 1210 +370	1100 rAspG1y3er GGATGGCAGC 1220	1110 +3- LyaAspSerC AAGGACTCCTI 1230 +3	1120 40 yalyaGlyAa GCAAGGGGGA 1240 80	1130 pSerGlyGly CAGTGGAGGO 1250	1140 +35 ProHisAleTh CCACATGCCAC 1260 +39	1150 orHieTyrar ocactacce 1270	1160 gGlyThrTrg GGGCACGTGG 1280	1170 +36 TyrLauThr61 TACCTGACGG 1290 +46	1180 50 LylleVelSe 5CATCGTCAC 1300 00	1190 orTrpG1yG1n ocTGGGGCCAG 1310 +406	1200 GlyCyall GGCTGCGC 1320
OCTGGGGGGAG 1090 +390 AleGlyTyr3e GOOGGCTACTO 1210 +370 ThrValGlyRi ACCGTGGGCCA	1100 rAspG1ySer GGATGGCAGC 1220 sPhsG1yVa1	1110 +34 LyaAspSerCt AAGGACTCCTT 1230 +3 TyrTbrArgV	1120 40 yalyagiyaa ccaagggga 1240 80 alserginty TCTCCCAGTA	1130 pperGlyGly CAGTGGAGGO 1250 rrlleGluTrp	1140 +35 ProBisAleTh ccacaTGCCAC 1260 +39 LeuGinLysLe CTGCAAAAGCT	1150 orHieTyrar ocactacce 1270	1160 gGlyThrTrg GGGCACGTGG 1280	1170 +36 TyrLauThr61 TACCTGACGG 1290 +46	1180 50 LylleVelSe 5CATCGTCAC 1300 00	1190 orTrpG1yG1n ocTGGGGCCAG 1310 +406	1200 GlyCyall GGCTGCGC 1320
OCTGGCGCAC 1090 •330 AleGlyTyrSe GCCGCTACTO 1210 •370 ThrValGlyBi ACCGTGGGCCA 1330	1100 rApp[1y3er GGATGGCAGC 1220 sPheG1yVe1 CTITGGGTG	1110 +3- LyaAapSerC AAGGACTCCTI 1230 +3 TyrThrArgV TACACCAGGG	1120 40 yalyagiyaa ccaagggga 1240 80 alserginty TCTCCCAGTA	1180 pSerGlyGly CAGTGGAGGO 1250 rrlleGluTrp CATCGAGTGG	1140 +35 ProHishleTh ccacaTGCCAC 1260 +39 LeuGinLysle CTGCAAAAGCT 1380	1150 O ITHISTYPAP COACTACCE 1270 O HIBSTATESETT 1390	1160 gG1yThrTr; ccGCACGTGC 1280 rG1uProAr; AGAGCCACG 1600	1170 -36 TYPLeuThr6 TACTGACGGG 1290 -46 PProGlyVelLe CCAGGAGTOC 1410	1180 50 1ylloWelSe 5CATCGTCAC 1300 00 euLeuArgAl TCCTGCGAGG 1420	1190 erTrpG1yG1m cCTGGGGCCAG 1310 +406 LeProPhePro CCCCATTTCCC 1430	1200 G1YCYAA1 GGCTGGGG 1320 TAGGGGGG
**************************************	TAPE 1 YEAR THE TA	1110 +3 LyaAspSerC AAGGACTOCTI 1230 +3 TyrThrArgV TACACCAGGG 1350	1120 40 yeLyeGlyAe 6CAAGGGGGA 1240 80 elSerGlnTy TCTCCCAGTA 1360	1180 specifyGly cagingaage 1250 rileGlutrp catogaging 1370 retoctegcag	1140 +35 ProHishlath CCACATECCAC 1260 +39 LeuGinLysle CTGCAAAAGCT 1380	1150 io arHieTyrArioccacTaccs 1270 io nulletArgSe rcaTaccctc 1390	1160 gGlyThrTx; GGGCACGTGG 1280 rGluProAr; AGAGCCACG 1400 GCAGTTAATI	1170 -36 STYPLEUTRES STACCTGACGG 1290 -46 SPPOGLYVALL COCAGGAGTOC 1410 CCCGGTAGAGGA	1180 50 1ylloWelSe 5CATCGTCAC 1300 00 euLeuArgAl TCCTGCGAGG 1420	1190 erTrpG1yG1m cCTGGGGCCAG 1310 +406 LeProPhePro CCCCATTTCCC 1430	1200 G1YCYAA1 GGCTGGGG 1320 TAGGGGGG
estecoccac 1090 •330 AlaGiyTyr5ac coccccTacTo 1210 •370 ThrValGiyRi acccTcccca 1330 AccccTcccct 1450	1100 rhapGlySer GGATGGCAGC 1220 ePheGlyVel CTTTGGGGTG 1340 GTGGAGAGAGAI 1460	1110 +3- LyaAspSerC: AAGGACTCCTI 1230 +3- TyrThrArgV TACACCAGGG 1350 AAGCCAAGGCT 1470	1120 40 yalysGlyAs GCAAGGGGA 1240 80 e1SerGlnTy TCTCCCAGTA 1360 ECGTCGAACT	1130 pSerGlyGly; cAGTGGAGGO 1250 r:IleGluTrp cATCGAGTGG 1370	1140 +35 ProHishleTh ccacataccac 1250 +39 LeuGinLyeLe CTGCAAAAGCT 1380 CCAAATCCCATA	1150 00 07HieTyxAr- 00CACTACOS 1270 00 00 00HietArgSe 1CATGOSCTC 1390 04TATTCTTCT 1510	1160 gGlyThrTr; gGGCACGTGC 1280 rGluProAr; aGaCCCACGG 1400 GCAGTTAATI 1520	1170 *36 STYPLOUTHF6 STYPLOUTHF6 STACCTGACGGG 1290 *44 SPROGLYVALL CCCAGGAGTOC* 1410 CCCGCTAGAGGA 1530	1180 50 1yTleVe15e 5CATCGTCAC 1300 00 eul.euArgAl TCCTGCGASC 1420 GGGCATGGG	1190 prTrpGlyGlm pcTrgGgGCAG 1210 +406 LeProPhePro ccccaTTTCCC 1430 AGGGAGGAGG	1200 G1yCysA1 GGCTGCGC 1320 TAGCCCAG 1440 AGGTGGGGA
estecoccac 1090 •330 AlaGiyTyr5ac coccccTacTo 1210 •370 ThrValGiyRi acccTcccca 1330 AccccTcccct 1450	1100 rhapGlySer GGATGGCAGC 1220 ePheGlyVel CTTTGGGGTG 1340 GTGGAGAGAGAI 1460	1110 +3- LyaAspSerC: AAGGACTCCTI 1230 +3- TyrThrArgV TACACCAGGG 1350 AAGCCAAGGCT 1470	1120 40 yalysGlyAs GCAAGGGGA 1240 80 e1SerGlnTy TCTCCCAGTA 1360 ECGTCGAACT	1130 pSerGlyGly; cAGTGGAGGO 1250 r:IleGluTrp cATCGAGTGG 1370	1140 +35 ProHishleTh ccacataccac 1250 +39 LeuGinLyeLe CTGCAAAAGCT 1380	1150 00 00 00 00 00 00 00 00 00 00 00 00 0	1160 gGlyThrTrj gGGCACGTGG 1280 rGluProAr; aGaGCCACGG 1400 GCAGTTAAT 1520 aGaGACTCA	1170 -38 http://withre-1 http:	1180 50 1yTleVe15e 5CATCGTCAC 1300 00 eul.euArgAl TCCTGCGASC 1420 GGGCATGGG	1190 prTrpGlyGlm pcTrgGgGCAG 1210 +406 LeProPhePro ccccaTTTCCC 1430 AGGGAGGAGG	1200 G1yCysA1 GGCTGCGC 1320 TAGCCCAG 1440 AGGTGGGGA
GETECOCCACO 1090 *330 AlaGiyTyr3m COCCCCTACTO 1210 *370 ThrValGiyHi ACCCTCGCCA 1330 ACCCCTCGCCA 1450 GEAGACAGAGA 1570	TANDETY SET GGATGGCAGC 1220 spheGlyVel CTTTGGGTE 1340 GTGGAGAGAA 1460 KCAGAAACAGI	1110 -3- LyaAmpGerCoom 1230 -3- TyrThrAmpCoom 1230 -3- TyrThrAmpCoom 1350 AGCCAAGGCT 1470 AGAGAGACAGA 1590	1120 40 40 40 yal.ya61yAa 6CAAGGGGA 1240 80 41SerG1mTy TCTCCCAGTA 1360 ECCTCGAACT 1480 GACAGAGAGG	1130 ppserGlyGly CACTGGAGGG 1250 rrIleGluTrp CATGGAGTGG 1370 retrocteGCAC 1490	1140 - 355 ProBiableTh ccacateccac 1250 - 595 LeuGinlysLe CTCASASGCT 1300 CCACATCCCATS 1500	1150 O INTHISTYRAN INCOMPTS 1270 INDISTANCE 1270 INDISTANCE 1390 ATATTCTTCT 1510 GGACATGGAE 1630	gGlyThrTry gGGCACGTGC 1280 rGluProAry aGAGCCACGG 1400 CCAGTTAATT 1520 AGAGACTCA	1170 -36 TYPLEUTHF6 TACCTGACGGG 1290 -44 PPFG1YVELL COCAGGAGTOC 1410 CCGGTAGAGGA 1530 AAGAGACTCCA 1650	1180 SO STATEMENT STATEMEN	al 190 pring lyGin	1200 G1YCYALI GGCTGCGC 1320 TAGCCCAC 1440 AGGTGGGGA 1360 GAGACACAC 1680
GETECOCCACO 1090 *330 AlaGiyTyr3m COCCCCTACTO 1210 *370 ThrValGiyHi ACCCTCGCCA 1330 ACCCCTCGCCA 1450 GEAGACAGAGA 1570	TANDETY SET GGATGGCAGC 1220 spheGlyVel CTTTGGGTE 1340 GTGGAGAGAA 1460 KCAGAAACAGI	1110 -3- LyaAmpGerCoom 1230 -3- TyrThrAmpCoom 1230 -3- TyrThrAmpCoom 1350 AGCCAAGGCT 1470 AGAGAGACAGA 1590	1120 40 40 40 yal.ya61yAa 6CAAGGGGA 1240 80 41SerG1mTy TCTCCCAGTA 1360 ECCTCGAACT 1480 GACAGAGAGG	1130 ppserGlyGly CACTGGAGGG 1250 rrIleGluTrp CATGGAGTGG 1370 retrocteGCAC 1490	1140 - 355 ProBiableTh ccacateccac 1250 - 595 LeuGinlysLe CTCASASGCT 1300 CCACATCCCATS 1500	1150 O INTHISTYRAN INCOMPTS 1270 INDISTANCE 1270 INDISTANCE 1390 ATATTCTTCT 1510 GGACATGGAE 1630	gGlyThrTry gGGCACGTGC 1280 rGluProAry aGAGCCACGG 1400 CCAGTTAATT 1520 AGAGACTCA	1170 -36 TYPLEUTHF6 TACCTGACGGG 1290 -44 PPFG1YVELL COCAGGAGTOC 1410 CCGGTAGAGGA 1530 AAGAGACTCCA 1650	1180 SO STATEMENT STATEMEN	al 190 pring lyGin	1200 G1YCYALI GGCTGCGC 1320 TAGCCCAC 1440 AGGTGGGGA 1360 GAGACACAC 1680
CETECOCICAD 1090 -330 AleGiyTyr3e COOSCCTACTO 1210 -370 ThrValGiyfii ACCCTCCCCC 1330 ACCCCTCCCCT 1450 CCAGACAGAGA 1370 CATGGATAGG	TABOE 195er GGATGGCAGC 1220 aPhaG19Val CTITGGGGTE 1340 GTGGAGAGAAA 1460 MAAGATGAGA	1110 1310 Sylvanapsaro Lyanapsaro 1230 Syrthrargy Thanacagga 1350 Lagocaaggat 1470 Lagocaaggat 1390 Lagocaaggat	1120 40 yalysGlyAs 6CAAGGGGGA 1240 80 wlSerGlmTy TCTCCAGTA 1360 ECGTCGAACT 1480 AGACAGAGAGGGGA 1600	1130 ppserGlyGly CACTGGAGGG 1250 rrIleGluTrp CATGGAGTGG 1370 retrocteGCAC 1490	1140 - 355 ProHishleTh ccacateccac 1250 - 595 LeuGinlysLe CTCCAAAAGCT 1300 CCAAATCCCATA 1500	1150 O INTHISTYRAN INCOMPTS 1270 INDISTANCE 1270 INDISTANCE 1390 ATATTCTTCT 1510 GGACATGGAE 1630	gGlyThrTry gGGCACGTGC 1280 rGluProAry aGAGCCACGG 1400 CCAGTTAATT 1520 AGAGACTCA	1170 -36 TYPLEUTHF6 TACCTGACGGG 1290 -44 PPFG1YVELL COCAGGAGTOC 1410 CCGGTAGAGGA 1530 AAGAGACTCCA 1650	1180 SO STATEMENT STATEMEN	al 190 pring lyGin	1200 G1YCYALI GGCTGCGC 1320 TAGCCCAC 1440 AGGTGGGGA 1360 GAGACACAC 1680
cerececcada 1999 -330 AlsGlyTyrds cooccracro 1210 -370 ThrysalGlyfil accerecect 1330 Accerecect 1350 Ceacacacacac 1370 Categartacacacac 1590	TABDE 193er GGATGGCAGC 1220 sPheG1yVe1 CTTTGGGGTE 1340 CTGGAGAGAACAGI 1380 AAAAGATGAGI 1700	1110 LyaAsparC AAGGACTOCTI 1230 STYTTHATSTY TACACCAGGG 1350 AGGCAAGGCT 1470 AGAGACACAGG 1590 AGGCAAGGGCGAGGGGGAGGGGGAGGGGGGGGGGGGGG	1120 40 yelysGlyAs GCAAGGGGGA 1240 80 elSerGlnTy TCTCCCAGTA 1360 CCGTCGAACT 1480 GACAGGAGGGG 1500 AGACAGGGGGCCCT 1720	pSerGlyGly cAGTGGAGGO 1250 rrIleGlutry cAGTGGTGG 1370 reTecteGGAC 1490 AGACTGAGGGA 1610	1140 ×355 ProHishleTh ccaca Teccac 1260 ×399 LeuGinLysie CTCCAAAAGCT 1380 CCAAATCCCATs 1300 AGAAATCCCATs 1300 CCCAGGGGAGTT 1740	1150 10 12H10TyrAr- 10CACTACOG- 1270 1270 1270 1270 1270 1270 1270 1270	gGlyThrTry segCacCTGG 1280 rGluProAry aGaSCCACCTAATI 1520 aGAGACTCA 1640 rtccttgaGG	1170 -36 TyrLeuThr6 TYrLeuThr6 T1290 -44 SPro61y9alt DCCACGACTOC 1410 DCCCTAGACGAC 1530 AAGACACTCCA 1550 CAGACAGCCCA 1770	1180 in 118Va 15e	1190 prTrpG1yG1n p	GIYCYALI GGCTGCGC 1320 TAGCCCAG 1440 AGGTGGGA 1560 AGGACACAG 1680 TTCAGCCAG 1800
CCTECCCCACC 1090 -330 AlsGlyTyr3e CCCCCTACTO 1210 -370 ThrValGlyRi aCCCTCCCCA 1330 ACCCTCCCCCA 1350 CCACACACACA 1370 CATGGATAGI 1590 CCCCCACCTCC	TABO 173er GGATGGCAGC 1220 PheG19Vel CTTTGGGTTC 1840 CTGGGGAAACAGG 1380 AAAAGATGAGG 1700 CAGGTGATGATTCTTC	LyakapSarC AAGGACTOCTI 1230 • 3 TyrThrArgV TTACACCAGG 1350 AGGCAAGGCT 1470 AGGGAGCAGGAG 1390 AGGCAAGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	1120 40 yal.yaG1yAa 6CAAGGGGA 80 a1SerG1nTy TCTCCCAGTA 1360 EGGTCGAACT 1480 AGACAGAGAGGGGA 1500 AGACAGGGGG	1130 pSerGlyGlyicaGTGGAGGG 1250 rClleGluTrp rClleGluTrp rCatCGAGTGG 1370 rCTCGCTGGAGGGAGGGAGGGAGGGGAGGGGAGGGGAGGG	1140 ×355 ProHishleTh ccaca Teccac 1260 ×399 -LeuGinLysle CTCCAAAAGCT 1380 CCAAATCCCATs 1300 CCAAATCCCATs 1500 CCCCCCCATS 1740 TTGCTGGAGACT	1150 or control of the control of th	1160 gciyThrTrp gcgCacctGc 1280 refulPreary asasccacce 1800 ccacTTAATI 1520 asasccacca asasccaccaccaccaccaccaccaccaccaccaccacca	1170 -36 TyrLeuThr6 TYrLeuThr6 T1290 -44 SPro61y9alt DCCACGACTOC 1410 DCCCTAGACGAC 1530 AAGACACTCCA 1550 CAGACAGCCCA 1770	1180 in 118Va 15e	1190 prTrpG1yG1n p	GIYCYALI GGCTGCGC 1320 TAGCCCAG 1440 AGGTGGGA 1560 AGGACACAG 1680 TTCAGCCAG 1800
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COTECCCCAN 1909 -330 AlsGlyTyr3= COCCCTACTO 1210 -370 ThrValGlyfil ACCTCCCCA 1330 ACCCTCCCCA 1370 CATCGAATAGL 1570 CATCGAATAGL 1690 CCCCCCCCCTCTC 1610	TABOT YEAR THOO TABOT YEAR GGATGGCAGC 1220 THOO THOO THOO THOO THOO THOO THOO THO	LyanapserC ANGACTOTT 1200 -3 TYPTTHEARTY THACACCAGG 1350 ANGECAAGGCT 1470 ANGAGACACAGA 1390 ANGAGACACAGA 1390 ANGAGACACAGA 1390 ANGAGACACAGA 1390 ANGAGACACAGA 1390 ANGAGACACAGA 1390 ANGAGACACAGA 1390 ANGAGACACAGA 1390	1120 60 yal.yaGiyAs CCAAGGGGGA 1240 80 salSerGinty TCTCCCAGTA 1360 GGGTGGAACT 1480 GGCAGAGGGGCC 1720 AGGCTGCTGC 1720 AGGCTGCTGC 1840	pSerGlyGly: CASTGGAGGO TZIIGGIUTEP CATGGAGGG 1370 TETOCTEGGAG 1490 AGACTGAGGGG 1730 TCCGCCTTCAI	1140 - 355 ProMissharts Caccaraccac 1250 - 393 Laudinlynds CTGCAAAAGCT 1380 - 394 CCAAAATCCCATA 1380 - 384 CCAAAATCCCATA 1380 - 384 CCAAAATCCCATA 1380 - 384 CCAAAATCCCATA 1380 - 384 CCAAACCACCACACCACACCACACCACACCACACCAC	1130 o or resident process of the control of the co	gGlyThrTry gGCGCACCTGC 1280 rG1uProAry aGAGCCACGC 1400 rC1uProAry 1520 rCACCTTAATT 1520 rCCACCTGAGG 1760 rTCCTGGAGG 1760 rTGACCACCACCACCACCACCACCACCACCACCACCACCACC	1170 -38 -37 -37 -37 -37 -37 -37 -37 -37 -37 -37	1180 Solve Television of the control	1190 PETFECT YOU	B200 G19Cyak1 GGCTGCGC 1320 TAGCCCGC 1360 AGGTGGGGA 1360 TTCAGCCA 1800 ACACACAG 1970
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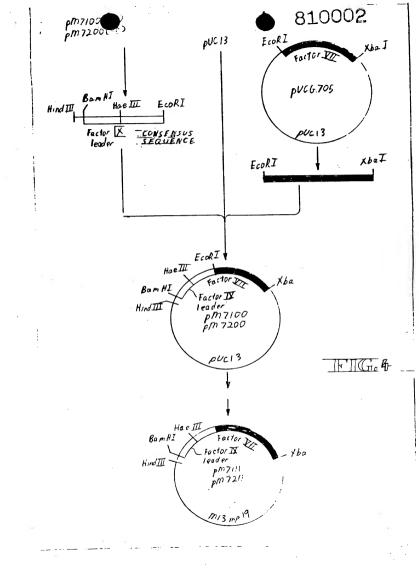
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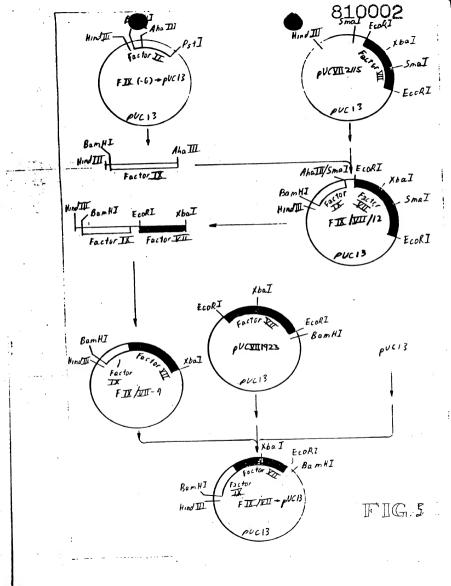
FIG. 28

cDNA Amino Acid Sequence

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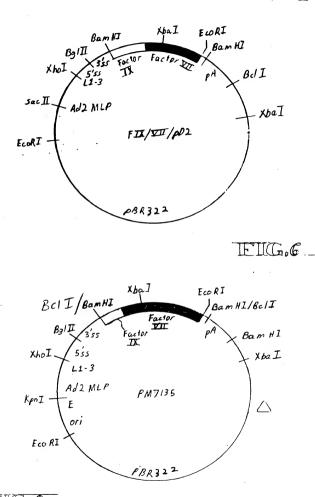


FIG.8

FIGURE 7

21 GGATCC ATG CAG CGC GTG AAC ATG ATC ATG GCA GAA TCA CCA GGC MET Gln Arg Val Asn MET lle MET Ala Glu Ser Pro Gly 66 CTC ATC ACC ATC TGC CIT TTA GGA TAT CTA CTC AGT GCT GAA TGT Leu 11e Thr 11e Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys 126 111 96 ACA GTT TTT CTT GAT CAT GAA AAC GCC AAC AAA ATT CTG AAT CGG Thr Val Phe Leu Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg CCA AAG AGG TAT AAT TCA GGT AAA TTG GAA GAG TTT GTT CAA GGG Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly 201 Asn Leu Glu Arg Glu Cys MET Glu Glu Lys Cys Ser Phe Glu Glu 261 246 231 GCA CGA GAA GTT TTT GAA AAC ACT GAA AGA ACA AAG CTG TTC TGG Ala Arg Glu Val Phe Glu Asn'Thr Glu Arg Thr Lys Leu Phe Trp 291 306 276 ATT TCT TAC AGT GAT GGG GAC CAG TGT GCC TCA AGT CCA TGC CAG Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln AAT GGG GGC TCC TGC AAG GAC CAG CTC CAG TCC TAT ATC TGC TTC Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe 396 381 366 TGC CTC CCT GCC TTC GAG GGC CGG AAC TGT GAG ACG CAC AAG GAT Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp 441 426 411 GAC CAG CTG ATC TGT GTG AAC GAG AAC GGC GGC TGT GAG CAG TAC Asp Glu Leu Ile Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr 486 471 TGC AGT GAC CAC ACG GGC ACC AAG CGC TCC TGT CGG TGC CAC GAG Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu 516 GGG TAC TCT CTG CTG GCA GAC GGG GIG TCC TGC ACA CCC ACA GTT Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro Thr Val 561 546 GAA TAT CCA TCT GGA AAA ATA CCT ATT CTA GAA AAA AGA AAT GCC Glu Tyr Pro Cys Gly Lys 1le Pro Ile Leu Glu Lys Arg Asn Ala 606 621 591 AGC AAA CCC CAA GGC CGA ATT GTG GGG GGC AAG GTG TGC CCC AAA

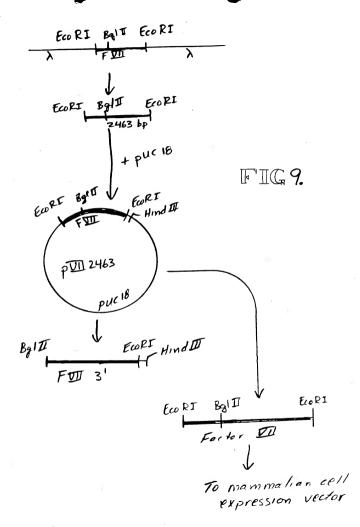
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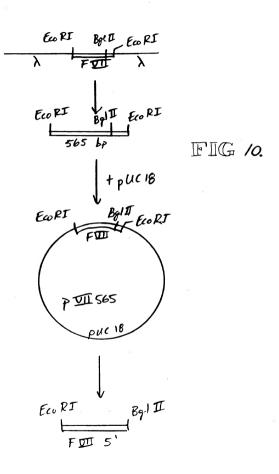
651 636 GGG GAG TGT CCA TGG CAG GTC CTG TTG TTG GTG AAT GGA GCT CAG Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln 711 696 681 TTG TGT GGG GGG ACC CTG ATC AAC ACC ATC TGG GTG GTC TCC GCG Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala 741 GCC CAC TGT TTC GAC AAA ATC AAG AAC TGG AGG AAC CTG ATC GCG Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala 771 786 GTG CTG GGC GAG CAC GAC CTC AGC GAG CAC GAC GGG GAT GAG CAG Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln 846 816 831 AGC CGG CGG GTG GCG CAG GTC ATC ATC CCC AGC ACG TAC GTC CCG Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro 891 861 876 GGC ACC ACC AAC CAC GAC ATC GCG CTG CTC CGC CTG CAC CAG CCC Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln Pro 906 921 GTG GTC CTC ACT GAC CAT GTG GTG CCC CTC TGC CTG CCC GAA CGG Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg 966 951 ACG TTC TCT GAG AGG ACG CTG GCC TTC GTG CGC TTC TCA TTG GTC Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val 1026 996 1011 AGC GGC TGG GGC CAG CTG CTG GAC CGT GGC GCC ACG GCC CTG GAG Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu 1071 1041 1056 CTC ATG GTC CTC AAC GTG CCC CGG CTG ATG ACC CAG GAC TGC CTG Leu MET Val Leu Asn Val Pro Arg Leu MET Thr Gln Asp Cys Leu 1116 1101 CAG CAG TCA CGG AAG GTG GGA GAC TCC CCA AAT ATC ACG GAG TAC Gln Gln Ser Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr 1161 1131 1146 ATG TTC TGT GCC GGC TAC TCG GAT GGC AGC AAG GAC TCC TGC AAG MET Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys 1206 1191 1176 GGG GAC AGT GGA GGC CCA CAT GCC ACC CAC TAC CGG GGC ACG TGG Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg Gly Thr Trp 1251 1236 1221 TAC CTG ACG GGC ATC GTC AGC TGG GGC CAG GGC TGC GCA ACC GTG Tyr Leu Thr gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val

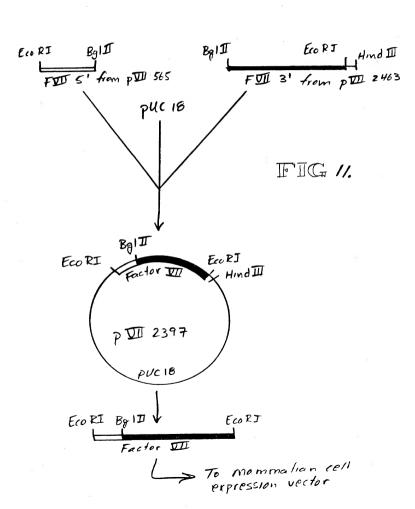
1281 1266 GGC CAC TIT GGG GTG TAC ACC AGG GTC TCC CAG TAC ATC GAG TGG Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp 1326 1341 1311 CTG CAA AAG CTC ATG CGC TCA GAG CCA CGC CCA GGA GTC CTC CTG Leu Gln Lys Leu MET Arg Ser Glu Pro Arg Pro Gly Val Leu Leu 1378 1388 1356 CGA GCC CCA TTT CCC TAG CCCAGCAGCC CTGGCCTGTG GAGAGAAAGC Arg Ala Pro Phe Pro . 1428 1438 1418 1408 CAAGGCTGCG TCGAACTGTC CTGGCACCAA ATCCCATATA TTCTTCTGCA 1458 1468 1478 1488 1498 GTTAATGGGG TAGAGGAGGG CATGGGAGGG AGGGAGGAGT GGGGAGGGAG 1508 1518 1528 1538 1558 1568 1578 1588 1598 ACTCTGAGGA CCATGGAGAG AGACTCAAAG AGACTCCAAG ATTCAAAGAG 1618 1628 1638 1608 ACTAATAGAG ACACAGAGAT GGAATAGAAA AGATGAGAG CAGAGGCAGA 1668 1678 1688 CAGGCGCTGG ACAGAGGGGC AGGGGAGTGC CAAGGTTGTC CTGGAGGCAG 1718 1728 1738 1748 1708 ACAGCCCAGC TGAGCCTCCT TACCTCCCTT CAGCCAAGCC CCACCTGCAC 1758 1768 1778 1788 GTGATCTGCT GGCCCTCAGG CTGCTGCTCT GCCTTCATTG CTGGAGACAG 1808 1818 1828 1838 1848 TAGAGGCATG ACACACATGG ATGCACACAC ACACACGCCA TGCACACACA 1858 1868 1878 1888 CAGAGATATG CACACACG GATGCACACA CAGATGGICA CACAGAGIAC 1918 1928 1938 1948

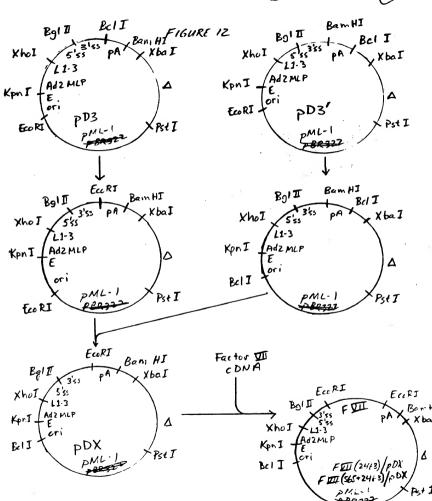
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1998	1988	978	TGCACG	1968	1958
CGCACACATC	TGCCAATGCA	ACA		ACACATGGAG	ACACAGATAT
2048	2038	028	GATATG	2018	2008
CGCACACACA	CACCGATGTG	CACA		GATGCACAGA	AGTGCACACG
2098	2088	2078	AGCACA	2068	2058
GCACACACAC	CACCAAGTGC	CACA		CACATGGATG	GATATGCACA
2148	2138	2128	ACACAG	2118	2108
ATGCTGACTC	ACACACACCG	ATGC		ACAGATGCAC	CGATGTACAC
2198	2188	2178	GGCGGT	2168	2158
TTTTCTGGTT	TAGCTCTCAC	TGTT		GTCCTCTGAA	CATGTGTGCT
2248	2238	2228	CTTCAC	2218	2208
TCACCATGCA	TTCAGAAGCA	ACAA		ATCATCTTCA	CTTATCCATT
2298	2288	2278	СТСТС	2268	2258
TCCCTTCGC1	AATGTATTTC	CCCA		TGCCCCCAAA	TGGTGGCGAA
2348	2338	2328	TATTC	2318	2308
GCTTCACAAT	CTGCTTCCCA	CCAC		CTGCACAGAC	GGGTGCCGGG
2398 AAAAAAAAA	2388 AAAAAAAAA	2378 AAAA	AAAAA	2368 GTCTCCTCG	2358
	2438 CCGGGGATCC	428		2418	2408









CGG ACG TTC TCT GAG AGG ACG CTG GCC TTC GTG CGC TTC TCA TTG GTC AGC GGC Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Nar I TEG GGC CAG CTG CTG BAC CGT GCC GCC ACG GCC CTG GAG CTC ATG GTC CTC AAC Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Het Val Leu Asn Pst Ib GTG CCC CGG CTG ATG ACC CAG GAC TGC CTG CAG CAG TCA CGG AAG GTG GGA GAC Val Pro Arg Leu Het Thr Gin Asp Cys Leu Gin Gin Ser Arg Lys Val Gly Asp TCC CCA AAT ATC ACG GAG TAC ATG TTC TGT GCC GGC TAC TCG GAT GGC AGC AAG Ser Pro Asn lie Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys GAC TCC TGC AAG GGG GAC AGT GGA GGC CCA CAT GCC ACC CAC TAC CGG GGC ACG Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg Gly Thr TGG TAC CTG ACG GGC ATC GTC AGC TGG GGC CAG GGC TGC GCA ACC GTG GGC CAC Trp Tyr Leu Thr Gly lie Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His 1059 TagI TTT GGG GTG TAC ACC AGG GTC TCC CAG TAC ATC GAG TGG CTG CAA AAG CTC ATG Phe Gly Val Tyr Thr Arg Val Ser Gin Tyr Ile Glu Trp Leu Gin Lys Leu Met CGC TCA GAG CCA CGC CCA GGA GTC CTC CTG:CGA GCC CCA.TTT.CCC TAG:CCCAGCAGCC Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro Pst Ic CTGGCCTGTG GAGAGAAAGC CAAGGCTGCG TCGAACTGTC CTGGCACCAA ATCCCATATA TTCTTCTGCA GTTAATGGGG TAGAGGAGGG CATGGGAGGGG AGGGAGGAGGT GGGGAGGGAG ACAGAGACAG AAACAGAGAG AGACAGAGAC AGAGAGAGAC TGAGGGAGAG ACTCTGAGGA CCATGGAGAG AGACTCAAAG AGACTCCAAG ATTEMAAGAG ACTAATAGAG ACACAGAGAT GGAATAGAAA AGATGAGAGG CAGAGGCAGA CAGGCGCTGG

ACAGAGGGGC AGGGGAGTGC CAAGGTTGTC CTGGAGGCAG ACAGCCCAGC TGAGCCTCCT TACCTCCCTT

1498 1508 1518 1528 1538 1548 1558
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1568 1578 1588 1598 1608 1618 1628
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1638 1648 1658 1668 1678 1688 1698
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1708 1718 1728 1738 1748 1758 1768
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1778 1788 1798 1808 1818 1828 1838
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1848 1858 1868 1878 1888 1898 1908
CACCAAGTGC GCACACACA CGATGTACAC ACAGATGCA CACACAGATGC ACACACACCG ATGCTGACTC

1918 1928 1938 1948 1958 1968 1978
CATGTGTGCT GTCCTCTGAA GGCGGTTGTT TAGCTCTCAC TTTTCTGGTT CTTATCCATT ATCATCTTCA

1988 1998 2008 2018 2028 2038 2048
CTICAGACAA TTCAGAAGCA TCACCATGCA TGGTGGCGAA TGCCCCCAAA CTCTCCCCCA AATGTATITC

2058 2068 2078 2088 2098 2108 2118
TECCTTEGET GGGTGCCGGG CTGCACAGAC TATTCCCCAC CTGCTTCCCA GCTTCACAAT AAACGGCTGC